

FILE 'MEDLINE, BIOSIS, CAPLUS' ENTERED AT 15:01:12 ON 16 NOV 2006

L1 2214 S ABCG2 OR BCRP
L2 869 S INDOLOCARBAZOLE
L3 13 S L1 AND L2
L4 7 DUP REMOVE L3 (6 DUPLICATES REMOVED)

FILE 'STNGUIDE' ENTERED AT 15:03:11 ON 16 NOV 2006

FILE 'MEDLINE, BIOSIS, CAPLUS' ENTERED AT 15:05:48 ON 16 NOV 2006

L5 14029 S C421A OR 421
L6 25 S L1 AND L5
L7 11 DUP REMOVE L6 (14 DUPLICATES REMOVED)

EAST Search History

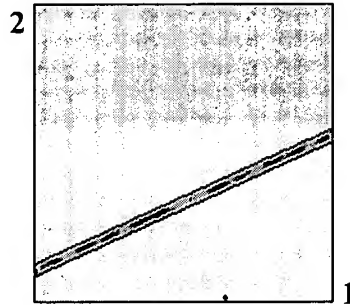
Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	197	ABCG2 or BCRP	US-PGPUB; USPAT; USOCR	OR	ON	2006/11/16 14:55
L2	318083	snp or mutation or polymorphism or variant	US-PGPUB; USPAT; USOCR	OR	ON	2006/11/16 14:55
L3	134	L1 and L2	US-PGPUB; USPAT; USOCR	OR	ON	2006/11/16 14:56
L4	140707	"421" or C421A	US-PGPUB; USPAT; USOCR	OR	ON	2006/11/16 14:56
L5	24	L1 and L2 and L4	US-PGPUB; USPAT; USOCR	OR	ON	2006/11/16 14:58
L6	28	L1 and L4	US-PGPUB; USPAT; USOCR	OR	ON	2006/11/16 14:59
L7	335	indolocarbazole	US-PGPUB; USPAT; USOCR	OR	ON	2006/11/16 14:59
L8	4	L1 and L7 and L2	US-PGPUB; USPAT; USOCR	OR	ON	2006/11/16 15:00

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.14 [May-07-2006]

Match: Mismatch: gap open: gap extension:
 x_dropoff: expect: wordsize: Filter ☒ View option
 Masking character option Masking color option
☐ Show CDS translation

Sequence 1: gi|44847528|emb|CQ757490.1|Sequence 1 from Patent WO2003107249.
 Length = 1968 (1 .. 1968)

Sequence 2: gi|62526032|ref|NM_004827.2|Homo sapiens ATP-binding cassette, sub-family G (WHITE), member 2 (ABCG2), mRNA
 Length = 4445 (1 .. 4445)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence.



4445

Score = 3757 bits (1954), Expect = 0.0
 Identities = 1968/1968 (100%), Gaps = 0/1968 (0%)
 Strand=Plus/Plus

Query 1 *seq id #1* ATGTCTTCCAGTAATGTCTGAAGTTTTTATCCCAGTGT CACAAGGAAACACCAATGGCTTC 60
 |||
 Sbjct 494 ATGTCTTCCAGTAATGTCTGAAGTTTTTATCCCAGTGT CACAAGGAAACACCAATGGCTTC 553
Zambet
 Query 61 CCCGCGACAGCTTCCAATGACCTGAAGGCATTTACTGAAGGAGCTGTGTTAAGTTTTTCAT 120
 |||
 Sbjct 554 CCCGCGACAGCTTCCAATGACCTGAAGGCATTTACTGAAGGAGCTGTGTTAAGTTTTTCAT 613
 Query 121 AACATCTGCTATCGAGTAAACTGAAGAGTGGCTTTCTACCTTGTCGAAAACCAAGTTGAG 180
 |||
 Sbjct 614 AACATCTGCTATCGAGTAAACTGAAGAGTGGCTTTCTACCTTGTCGAAAACCAAGTTGAG 673
 Query 181 AAAGAAATATTATCGAATATCAATGGGATCATGAAACCTGGTCTCAACGCCATCCTGGGA 240
 |||
 Sbjct 674 AAAGAAATATTATCGAATATCAATGGGATCATGAAACCTGGTCTCAACGCCATCCTGGGA 733
 Query 241 CCCACAGGTGGAGGCAAATCTTCGTTATTAGATGTCTTAGCTGCAAGGAAAGATCCAAGT 300

Sbjct	734	 CCCACAGGTGGAGGCAAATCTTCGTTATTAGATGTCTTAGCTGCAAGGAAAGATCCAAGT	793
Query	301	GGATTATCTGGAGATGTTCTGATAAATGGAGCACCGCGACCTGCCAATTTCAAATGTAAT 	360
Sbjct	794	GGATTATCTGGAGATGTTCTGATAAATGGAGCACCGCGACCTGCCAATTTCAAATGTAAT	853
Query	361	TCAGGTTACGTGGTACAAGATGATGTTGTGATGGGCACTCTGACGGTGAGAGAAAACCTTA 	420
Sbjct	854	TCAGGTTACGTGGTACAAGATGATGTTGTGATGGGCACTCTGACGGTGAGAGAAAACCTTA	913
Query	421	CAGTTCTCAGCAGCTCTTCGGCTTGCAACAACATGACGAATCATGnnnnnnnnCGAACGG 	480
Sbjct	914	CAGTTCTCAGCAGCTCTTCGGCTTGCAACAACATGACGAATCATGAAAAAACGAACGG	973
Query	481	ATTAACAGGGTCATTCAAGAGTTAGGTCTGGATAAAGTGGCAGACTCCAAGGTTGGAACCT 	540
Sbjct	974	ATTAACAGGGTCATTCAAGAGTTAGGTCTGGATAAAGTGGCAGACTCCAAGGTTGGAACCT	1033
Query	541	CAGTTTATCCGTGGTGTGTCTGGAGGAGAAAGAAAAAGGACTAGTATAGGAATGGAGCTT 	600
Sbjct	1034	CAGTTTATCCGTGGTGTGTCTGGAGGAGAAAGAAAAAGGACTAGTATAGGAATGGAGCTT	1093
Query	601	ATCACTGATCCTTCCATCTTGTTCTTGGATGAGCCTACAACCTGGCTTAGACTCAAGCACA 	660
Sbjct	1094	ATCACTGATCCTTCCATCTTGTTCTTGGATGAGCCTACAACCTGGCTTAGACTCAAGCACA	1153
Query	661	GCAAATGCTGTCCTTTTGCTCCTGAAAAGGATGTCTAAGCAGGGACGAACAATCATCTTC 	720
Sbjct	1154	GCAAATGCTGTCCTTTTGCTCCTGAAAAGGATGTCTAAGCAGGGACGAACAATCATCTTC	1213
Query	721	TCCATTTCATCAGCCTCGATATTCCATCTTCAAGTTGTTTGATAGCCTCACCTTATTGGCC 	780
Sbjct	1214	TCCATTTCATCAGCCTCGATATTCCATCTTCAAGTTGTTTGATAGCCTCACCTTATTGGCC	1273
Query	781	TCAGGAAGACTTATGTTCCACGGGCCTGCTCAGGAGGCCTTGGGATACTTTGAATCAGCT 	840
Sbjct	1274	TCAGGAAGACTTATGTTCCACGGGCCTGCTCAGGAGGCCTTGGGATACTTTGAATCAGCT	1333
Query	841	GGTTATCACTGTGAGGCCTATAATAACCCTGCAGACTTCTTCTTGGACATCATTAAATGGA 	900
Sbjct	1334	GGTTATCACTGTGAGGCCTATAATAACCCTGCAGACTTCTTCTTGGACATCATTAAATGGA	1393
Query	901	GATTCCACTGCTGTGGCATTAAACAGAGAAGAAGACTTTAAAGCCACAGAGATCATAGAG 	960
Sbjct	1394	GATTCCACTGCTGTGGCATTAAACAGAGAAGAAGACTTTAAAGCCACAGAGATCATAGAG	1453
Query	961	CCTTCCAAGCAGGATAAGCCACTCATAGAAAAATTAGCGGAGATTTATGTCAACTCCTCC 	1020
Sbjct	1454	CCTTCCAAGCAGGATAAGCCACTCATAGAAAAATTAGCGGAGATTTATGTCAACTCCTCC	1513
Query	1021	TTCTACAAAGAGACAAAAGCTGAATTACATCAACTTTCCGGGGGTGAGAAGAAGAAGAAG 	1080
Sbjct	1514	TTCTACAAAGAGACAAAAGCTGAATTACATCAACTTTCCGGGGGTGAGAAGAAGAAGAAG	1573
Query	1081	ATCACAGTCTTCAAGGAGATCAGCTACACCACCTCCTTCTGTTCATCAACTCAGATGGGTT 	1140
Sbjct	1574	ATCACAGTCTTCAAGGAGATCAGCTACACCACCTCCTTCTGTTCATCAACTCAGATGGGTT	1633
Query	1141	TCCAAGCGTTCATTCAAAAACCTTGCTGGGTAATCCCCAGGCCTCTATAGCTCAGATCATT 	1200
Sbjct	1634	TCCAAGCGTTCATTCAAAAACCTTGCTGGGTAATCCCCAGGCCTCTATAGCTCAGATCATT	1693
Query	1201	GTCACAGTCGTAAGTGGGACTGGTTATAGGTGCCATTTACTTTGGGCTAAAAAATGATTCT 	1260
Sbjct	1694	GTCACAGTCGTAAGTGGGACTGGTTATAGGTGCCATTTACTTTGGGCTAAAAAATGATTCT	1753

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Query 1261 ACTGGAATCCAGAACAGAGCTGGGGTTCTCTTCTTCCTGACGACCAACCAGTGTTCAGC 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1754 ACTGGAATCCAGAACAGAGCTGGGGTTCTCTTCTTCCTGACGACCAACCAGTGTTCAGC 1813

Query 1321 AGTGTTCAGCCGTGGAACCTCTTTGTGGTAGAGAAGAAGCTCTTCATACATGAATACATC 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1814 AGTGTTCAGCCGTGGAACCTCTTTGTGGTAGAGAAGAAGCTCTTCATACATGAATACATC 1873

Query 1381 AGCGGATACTACAGAGTGTCTATCTTATTTTCCTTGGAAAACGTATCTGATTTATTACCC 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1874 AGCGGATACTACAGAGTGTCTATCTTATTTTCCTTGGAAAACGTATCTGATTTATTACCC 1933

Query 1441 ATGAGGATGTTACCAAGTATTATATTTACCTGTATAGTGTACTTCATGTTAGGATTGAAG 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1934 ATGAGGATGTTACCAAGTATTATATTTACCTGTATAGTGTACTTCATGTTAGGATTGAAG 1993

Query 1501 CCAAAGGCAGATGCCTTCTTCGTTATGATGTTTACCCTTATGATGGTGGCTTATTACGCC 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1994 CCAAAGGCAGATGCCTTCTTCGTTATGATGTTTACCCTTATGATGGTGGCTTATTACGCC 2053

Query 1561 AGTTCCATGGCACTGGCCATAGCAGCAGGTGAGAGTGTGGTTTCTGTAGCAACACTTCTC 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 2054 AGTTCCATGGCACTGGCCATAGCAGCAGGTGAGAGTGTGGTTTCTGTAGCAACACTTCTC 2113

Query 1621 ATGACCATCTGTTTTGTGTTTATGATGATTTTTTCAGGTCTGTTGGTCAATCTCACAACC 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 2114 ATGACCATCTGTTTTGTGTTTATGATGATTTTTTCAGGTCTGTTGGTCAATCTCACAACC 2173

Query 1681 ATTGCATCTTGGCTGTCATGGCTTCAGTACTTCAGCATTCCACGATATGGATTTACGGCT 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 2174 ATTGCATCTTGGCTGTCATGGCTTCAGTACTTCAGCATTCCACGATATGGATTTACGGCT 2233

Query 1741 TTGCAGCATAATGAATTTTTTGGGACAAAACCTTCTGCCAGGACTCAATGCAACAGGAAAC 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 2234 TTGCAGCATAATGAATTTTTTGGGACAAAACCTTCTGCCAGGACTCAATGCAACAGGAAAC 2293

Query 1801 AATCCTTGTAACATATGCAACATGTACTGGCGAAGAATATTTGGTAAAGCAGGGCATCGAT 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 2294 AATCCTTGTAACATATGCAACATGTACTGGCGAAGAATATTTGGTAAAGCAGGGCATCGAT 2353

Query 1861 CTCTCACCTGGGGCTTGTGGAAGAATCACGTGGCCTTGGCTTGTATGATTGTTATTTTC 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 2354 CTCTCACCTGGGGCTTGTGGAAGAATCACGTGGCCTTGGCTTGTATGATTGTTATTTTC 2413

Query 1921 CTCACAATTGCCTACCTGAAATTGTTATTTCTTAAAAAATATTCTTAA 1968
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 2414 CTCACAATTGCCTACCTGAAATTGTTATTTCTTAAAAAATATTCTTAA 2461

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CPU time: 0.03 user secs. 0.01 sys. secs 0.04 total secs.

Lambda K H
1.33 0.621 1.12

Gapped
Lambda K H
1.33 0.621 1.12

Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Sequences: 1
Number of Hits to DB: 608
Number of extensions: 9
Number of successful extensions: 1
Number of sequences better than 10.0: 1

Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 1968
Length of database: 18,419,680,154
Length adjustment: 27
Effective length of query: 1941
Effective length of database: 18,419,680,127
Effective search space: 35752599126507
Effective search space used: 35752599126507
X1: 11 (21.1 bits)
X2: 26 (50.0 bits)
X3: 26 (50.0 bits)
S1: 15 (29.5 bits)
S2: 22 (43.0 bits)